

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 09/301,380A
Source: 1FW16
Date Processed by STIC: 6/2/06

ENTERED

CRF Errors Edited by the STIC Systems Branch

Serial Number: 09/301,380A

CRF Edit Date: 6/2/06
Edited by: AC

___ Realigned nucleic acid/amino acid numbers/text in cases where the sequence text "wrapped" to the next line

___ Corrected the SEQ ID NO. Sequence numbers edited were:

___ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

___ Deleted: ___ invalid beginning/end-of-file text ; ___ page numbers

___ Inserted mandatory headings/numeric identifiers, specifically:

___ Moved responses to same line as heading/numeric identifier, specifically:

✓
___ Other:

deleted number under stop codon - sequence 1
sequence 2 - corrected amino acid numbering



IFW16

RAW SEQUENCE LISTING

DATE: 06/02/2006

PATENT APPLICATION: US/09/301,380A

TIME: 09:38:41

Input Set : A:\PTO.txt

Output Set: N:\CRF4\06022006\I301380A.raw

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3 <110> APPLICANT: Murphy, Gerald P.
4     Boynton, Alton L.
5     Sehgal, Anil
7 <120> TITLE OF INVENTION: Nr-CAM GENE, NUCLEIC ACIDS AND NUCLEIC ACID PRODUCTS
8     FOR THERAPEUTIC AND DIAGNOSTIC USES FOR TUMORS
10 <130> FILE REFERENCE: 20093A-002100US
12 <140> CURRENT APPLICATION NUMBER: 09/301,380A
C--> 13 <141> CURRENT FILING DATE: 2001-06-15
15 <150> PRIOR APPLICATION NUMBER: 60/112,098
16 <151> PRIOR FILING DATE: 1998-12-14
18 <150> PRIOR APPLICATION NUMBER: 60/083,152
19 <151> PRIOR FILING DATE: 1998-04-27
21 <160> NUMBER OF SEQ ID NOS: 33
23 <170> SOFTWARE: PatentIn Ver. 2.0
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 4134
27 <212> TYPE: DNA
28 <213> ORGANISM: Homo sapiens
30 <220> FEATURE:
31 <221> NAME/KEY: CDS
32 <222> LOCATION: (130)..(4029)
34 <400> SEQUENCE: 1
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37 ttgtgaaaga agaaaaggaa attcagtgtg tgagtctcag caggagttaa gctaatacag 120
39 cttaaaata atg ccg aaa aag aag cgc tta tct gcg ggc aga gtg ccc ctg 171
40     Met Pro Lys Lys Lys Arg Leu Ser Ala Gly Arg Val Pro Leu
41         1             5             10
43 att ctc ttc ctg tgc cag atg att agt gca ctg gaa gta cct ctt gat 219
44 Ile Leu Phe Leu Cys Gln Met Ile Ser Ala Leu Glu Val Pro Leu Asp
45 15             20             25             30
47 cca aaa ctt ctt gaa gac ttg gta cag cct cca acc atc acc caa cag 267
48 Pro Lys Leu Leu Glu Asp Leu Val Gln Pro Pro Thr Ile Thr Gln Gln
49             35             40             45
51 tct cca aaa gat tac att att gac cct cgg gag aat att gta atc cag 315
52 Ser Pro Lys Asp Tyr Ile Ile Asp Pro Arg Glu Asn Ile Val Ile Gln
53             50             55             60
55 tgt gaa gcc aaa ggg aaa ccg ccc cca agc ttt tcc tgg acc cgt aat 363
56 Cys Glu Ala Lys Gly Lys Pro Pro Pro Ser Phe Ser Trp Thr Arg Asn
57             65             70             75
59 ggg act cat ttt gac atc gat aaa gac cct ctg gtc acc atg aag cct 411
60 Gly Thr His Phe Asp Ile Asp Lys Asp Pro Leu Val Thr Met Lys Pro
61             80             85             90
63 ggc aca gga acg ctc ata att aac atc atg agc gaa ggg aaa gct gag 459

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65 95 100 105 110
67 acc tat gaa gga gtc tat cag tgt aca gca agg aac gaa cgc gga gct 507
68 Thr Tyr Glu Gly Val Tyr Gln Cys Thr Ala Arg Asn Glu Arg Gly Ala
69 115 120 125
71 gca gtt tct aat aac att gtt gtc cgc cca tcc aga tca cca ttg tgg 555
72 Ala Val Ser Asn Asn Ile Val Val Arg Pro Ser Arg Ser Pro Leu Trp
73 130 135 140
75 acc aaa gaa aaa ctt gaa cca atc aca ctt caa agt ggt cag tct tta 603
76 Thr Lys Glu Lys Leu Glu Pro Ile Thr Leu Gln Ser Gly Gln Ser Leu
77 145 150 155
79 gta ctt ccc tgc aga ccc cca att gga tta cca cca cct ata ata ttt 651
80 Val Leu Pro Cys Arg Pro Pro Ile Gly Leu Pro Pro Pro Ile Ile Phe
81 160 165 170
83 tgg atg gat aat tcc ttt caa aga ctt cca caa agt gag aga gtt tct 699
84 Trp Met Asp Asn Ser Phe Gln Arg Leu Pro Gln Ser Glu Arg Val Ser
85 175 180 185 190
87 caa ggt ttg aat ggg gac ctt tat ttt tcc aat gtc ctc cca gag gac 747
88 Gln Gly Leu Asn Gly Asp Leu Tyr Phe Ser Asn Val Leu Pro Glu Asp
89 195 200 205
91 acc cgc gaa gac tat atc tgt tat gct aga ttt aat cat act caa acc 795
92 Thr Arg Glu Asp Tyr Ile Cys Tyr Ala Arg Phe Asn His Thr Gln Thr
93 210 215 220
95 ata cag cag aag caa cct att tct gtg aag gtg att tca gtg gat gaa 843
96 Ile Gln Gln Lys Gln Pro Ile Ser Val Lys Val Ile Ser Val Asp Glu
97 225 230 235
99 ttg aat gac act ata gct gct aat ttg agt gac act gag ttt tat ggt 891
100 Leu Asn Asp Thr Ile Ala Ala Asn Leu Ser Asp Thr Glu Phe Tyr Gly
101 240 245 250
103 gct aaa tca agt aga gag agg cca cca aca ttt tta act cca gaa ggc 939
104 Ala Lys Ser Ser Arg Glu Arg Pro Pro Thr Phe Leu Thr Pro Glu Gly
105 255 260 265 270
107 aat gca agt aac aaa gag gaa tta aga gga aat gtg ctt tca ctg gag 987
108 Asn Ala Ser Asn Lys Glu Glu Leu Arg Gly Asn Val Leu Ser Leu Glu
109 275 280 285
111 tgc att gca gaa gga ctg cct acc cca att att tac tgg gca aag gaa 1035
112 Cys Ile Ala Glu Gly Leu Pro Thr Pro Ile Ile Tyr Trp Ala Lys Glu
113 290 295 300
115 gat gga atg cta ccc aaa aac agg aca gtt tat aag aac ttt gag aaa 1083
116 Asp Gly Met Leu Pro Lys Asn Arg Thr Val Tyr Lys Asn Phe Glu Lys
117 305 310 315
119 acc ttg cag atc att cat gtt tca gaa gca gac tct gga aat tac caa 1131
120 Thr Leu Gln Ile Ile His Val Ser Glu Ala Asp Ser Gly Asn Tyr Gln
121 320 325 330
123 tgt ata gca aaa aat gca tta gga gcc atc cac cat acc att tct gtt 1179
124 Cys Ile Ala Lys Asn Ala Leu Gly Ala Ile His His Thr Ile Ser Val
125 335 340 345 350
127 aga gtt aaa gcg gct cca tac tgg atc aca gcc cct caa aat ctt gtg 1227
128 Arg Val Lys Ala Ala Pro Tyr Trp Ile Thr Ala Pro Gln Asn Leu Val

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133		370		375		380	
135	ccc aaa ccc aga att agc tgg tta aca aat gga gtc cca ata gaa att	1323					
136	Pro Lys Pro Arg Ile Ser Trp Leu Thr Asn Gly Val Pro Ile Glu Ile						
137		385		390		395	
139	gcc cct gat gac ccc agc aga aaa ata gat ggc gat acc att att ttt	1371					
140	Ala Pro Asp Asp Pro Ser Arg Lys Ile Asp Gly Asp Thr Ile Ile Phe						
141		400		405		410	
143	tca aat gtt caa gaa aga tca agt gca gta tat cag tgc aat gcc tct	1419					
144	Ser Asn Val Gln Glu Arg Ser Ser Ala Val Tyr Gln Cys Asn Ala Ser						
145	415		420		425		430
147	aat gaa tat gga tat tta ctg gca aac gca ttt gta aat gtg ctg gct	1467					
148	Asn Glu Tyr Gly Tyr Leu Leu Ala Asn Ala Phe Val Asn Val Leu Ala						
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151	gag cca cca cga atc ctc aca cct gca aac aca ctc tac cag gtc att	1515					
152	Glu Pro Pro Arg Ile Leu Thr Pro Ala Asn Thr Leu Tyr Gln Val Ile						
153		450		455		460	
155	gca aac agg cct gct tta cta gac tgt gcc ttc ttt ggg tct cct ctc	1563					
156	Ala Asn Arg Pro Ala Leu Leu Asp Cys Ala Phe Phe Gly Ser Pro Leu						
157		465		470		475	
159	cca acc atc gag tgg ttt aaa gga gct aaa gga agt gct ctt cat gaa	1611					
160	Pro Thr Ile Glu Trp Phe Lys Gly Ala Lys Gly Ser Ala Leu His Glu						
161		480		485		490	
163	gat att tat gtt tta cat gaa aat gga act ttg gaa atc aaa gat gct	1659					
164	Asp Ile Tyr Val Leu His Glu Asn Gly Thr Leu Glu Ile Lys Asp Ala						
165	495		500		505		510
167	aca tgg atc gtt aaa gaa att cct gtg gcc caa aag gac agt aca gga	1707					
168	Thr Trp Ile Val Lys Glu Ile Pro Val Ala Gln Lys Asp Ser Thr Gly						
169		515		520		525	
171	act tat acg tgt gtt gca agg aat aaa tta ggg atg gca aag aat gaa	1755					
172	Thr Tyr Thr Cys Val Ala Arg Asn Lys Leu Gly Met Ala Lys Asn Glu						
173		530		535		540	
175	gtt cac tta cag ccc gaa tat gca gtt gtg caa aga ggg agc atg gtg	1803					
176	Val His Leu Gln Pro Glu Tyr Ala Val Val Gln Arg Gly Ser Met Val						
177		545		550		555	
179	tcc ttt gaa tgc aaa gtg aaa cat gat cac acc tta tcc ctc act gtc	1851					
180	Ser Phe Glu Cys Lys Val Lys His Asp His Thr Leu Ser Leu Thr Val						
181		560		565		570	
183	ctg tgg ctg aag gac aac agg gaa ctg ccc agt gat gaa agg ttc act	1899					
184	Leu Trp Leu Lys Asp Asn Arg Glu Leu Pro Ser Asp Glu Arg Phe Thr						
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187	gtt gac aag gat cat cta gtg gta gct gat gtc agt gac gat gac agc	1947					
188	Val Asp Lys Asp His Leu Val Val Ala Asp Val Ser Asp Asp Asp Ser						
189		595		600		605	
191	ggg acc tac acg tgt gtg gcc aac acc act ctg gac agc gtc tcc gcc	1995					
192	Gly Thr Tyr Thr Cys Val Ala Asn Thr Thr Leu Asp Ser Val Ser Ala						
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199	tac	gat	gtc	cca	aat	cct	ccc	ttt	gac	tta	gaa	ctg	aca	gat	caa	ctt	2091
200	Tyr	Asp	Val	Pro	Asn	Pro	Pro	Phe	Asp	Leu	Glu	Leu	Thr	Asp	Gln	Leu	
201			640					645					650				
203	gac	aaa	agt	ggt	cag	ctg	tca	tgg	acc	cca	ggc	gat	gac	aac	aat	agc	2139
204	Asp	Lys	Ser	Val	Gln	Leu	Ser	Trp	Thr	Pro	Gly	Asp	Asp	Asn	Asn	Ser	
205	655					660					665					670	
207	ccc	att	aca	aaa	ttc	atc	atc	gaa	tat	gaa	gat	gca	atg	cac	aag	cca	2187
208	Pro	Ile	Thr	Lys	Phe	Ile	Ile	Glu	Tyr	Glu	Asp	Ala	Met	His	Lys	Pro	
209					675					680						685	
211	ggg	ctg	tgg	cac	cac	caa	act	gaa	ggt	tct	gga	aca	cag	acc	aca	gcc	2235
212	Gly	Leu	Trp	His	His	Gln	Thr	Glu	Val	Ser	Gly	Thr	Gln	Thr	Thr	Ala	
213				690						695						700	
215	cag	ctg	aag	ctg	tct	cct	tac	gtg	aac	tac	tcc	ttc	cgc	gtg	atg	gca	2283
216	Gln	Leu	Lys	Leu	Ser	Pro	Tyr	Val	Asn	Tyr	Ser	Phe	Arg	Val	Met	Ala	
217			705					710					715				
219	gtg	aac	agc	att	ggg	aag	agc	ttg	ccc	agc	gag	gcg	tct	gag	cag	tat	2331
220	Val	Asn	Ser	Ile	Gly	Lys	Ser	Leu	Pro	Ser	Glu	Ala	Ser	Glu	Gln	Tyr	
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223	ttg	acg	aaa	gcc	tca	gaa	cca	gat	aaa	aac	ccc	aca	gct	gtg	gaa	gga	2379
224	Leu	Thr	Lys	Ala	Ser	Glu	Pro	Asp	Lys	Asn	Pro	Thr	Ala	Val	Glu	Gly	
225	735					740					745					750	
227	ctg	gga	tca	gag	cct	gat	aat	ttg	gag	att	acg	tgg	aag	ccc	ttg	aat	2427
228	Leu	Gly	Ser	Glu	Pro	Asp	Asn	Leu	Glu	Ile	Thr	Trp	Lys	Pro	Leu	Asn	
229						755					760					765	
231	ggt	ttc	gaa	tct	aat	ggg	cca	ggc	ctt	cag	tac	aaa	ggt	agc	tgg	cgc	2475
232	Gly	Phe	Glu	Ser	Asn	Gly	Pro	Gly	Leu	Gln	Tyr	Lys	Val	Ser	Trp	Arg	
233						770					775					780	
235	cag	aaa	gat	ggt	gat	gat	gaa	tgg	aca	tct	gtg	ggt	gtg	gca	aat	gta	2523
236	Gln	Lys	Asp	Gly	Asp	Asp	Glu	Trp	Thr	Ser	Val	Val	Val	Ala	Asn	Val	
237								790								795	
239	tcc	aaa	tat	att	gtc	tca	ggc	acg	cca	acc	ttt	ggt	cca	tac	ctg	atc	2571
240	Ser	Lys	Tyr	Ile	Val	Ser	Gly	Thr	Pro	Thr	Phe	Val	Pro	Tyr	Leu	Ile	
241			800				805						810				
243	aaa	ggt	cag	gcc	ctg	aat	gac	atg	ggg	ttt	gcc	ccc	gag	cca	gct	gta	2619
244	Lys	Val	Gln	Ala	Leu	Asn	Asp	Met	Gly	Phe	Ala	Pro	Glu	Pro	Ala	Val	
245	815					820					825					830	
247	gtc	atg	gga	cat	tct	gga	gaa	gac	ctc	cca	atg	gtg	gct	cct	ggg	aac	2667
248	Val	Met	Gly	His	Ser	Gly	Glu	Asp	Leu	Pro	Met	Val	Ala	Pro	Gly	Asn	
249						835					840					845	
251	gtg	cgt	gtg	aat	gtg	gtg	aac	agt	acc	tta	gcc	gag	gtg	cac	tgg	gac	2715
252	Val	Arg	Val	Asn	Val	Val	Asn	Ser	Thr	Leu	Ala	Glu	Val	His	Trp	Asp	
253						850					855					860	
255	cca	gta	cct	ctg	aaa	agc	atc	cga	gga	cac	cta	caa	ggc	tat	cgg	att	2763
256	Pro	Val	Pro	Leu	Lys	Ser	Ile	Arg	Gly	His	Leu	Gln	Gly	Tyr	Arg	Ile	
257						865							875				
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264	Glu	Lys	Lys	Ile	Leu	Thr	Phe	Gln	Gly	Ser	Lys	Thr	His	Gly	Met	Leu	
265	895					900					905					910	
267	ccg	ggg	cta	gag	ccc	ttt	agc	cac	tac	aca	ctg	aat	gtc	cga	gtg	gtc	2907
268	Pro	Gly	Leu	Glu	Pro	Phe	Ser	His	Tyr	Thr	Leu	Asn	Val	Arg	Val	Val	
269					915					920					925		
271	aat	ggg	aaa	ggg	gag	ggc	cca	gcc	agc	cct	gac	aga	gtc	ttt	aat	act	2955
272	Asn	Gly	Lys	Gly	Glu	Gly	Pro	Ala	Ser	Pro	Asp	Arg	Val	Phe	Asn	Thr	
273				930					935					940			
275	cca	gaa	gga	gtc	ccc	agt	gct	ccc	tcg	tct	ttg	aag	att	gtg	aat	cca	3003
276	Pro	Glu	Gly	Val	Pro	Ser	Ala	Pro	Ser	Ser	Leu	Lys	Ile	Val	Asn	Pro	
277			945					950					955				
279	aca	ctg	gac	tct	ctc	act	ttg	gaa	tgg	gat	cca	ccg	agc	cac	ccg	aat	3051
280	Thr	Leu	Asp	Ser	Leu	Thr	Leu	Glu	Trp	Asp	Pro	Pro	Ser	His	Pro	Asn	
281		960					965				970						
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284	Gly	Ile	Leu	Thr	Glu	Tyr	Thr	Leu	Lys	Tyr	Gln	Pro	Ile	Asn	Ser	Thr	
285	975					980					985					990	
287	cat	gaa	tta	ggc	cct	ctg	gta	gat	ttg	aaa	att	cct	gcc	aac	aag	aca	3147
288	His	Glu	Leu	Gly	Pro	Leu	Val	Asp	Leu	Lys	Ile	Pro	Ala	Asn	Lys	Thr	
289				995					1000					1005			
291	cgg	tgg	act	tta	aaa	aat	tta	aat	ttc	agc	act	cga	tat	aag	ttt	tat	3195
292	Arg	Trp	Thr	Leu	Lys	Asn	Leu	Asn	Phe	Ser	Thr	Arg	Tyr	Lys	Phe	Tyr	
293			1010						1015				1020				
295	ttc	tat	gca	caa	aca	tca	gca	gga	tca	gga	agt	caa	att	aca	gag	gaa	3243
296	Phe	Tyr	Ala	Gln	Thr	Ser	Ala	Gly	Ser	Gly	Ser	Gln	Ile	Thr	Glu	Glu	
297			1025					1030				1035					
299	gca	gta	aca	act	gtg	gat	gaa	gct	ggg	att	ctt	cca	cct	gat	gta	ggg	3291
300	Ala	Val	Thr	Thr	Val	Asp	Glu	Ala	Gly	Ile	Leu	Pro	Pro	Asp	Val	Gly	
301		1040					1045				1050						
303	gca	ggc	aaa	gtt	caa	gct	gta	aat	acc	agg	atc	agc	aat	ctt	act	gct	3339
304	Ala	Gly	Lys	Val	Gln	Ala	Val	Asn	Thr	Arg	Ile	Ser	Asn	Leu	Thr	Ala	
305	1055				1060					1065				1070			
307	gca	gct	gct	gag	acc	tat	gcc	aat	atc	agt	tgg	gaa	tat	gag	gga	cca	3387
308	Ala	Ala	Ala	Glu	Thr	Tyr	Ala	Asn	Ile	Ser	Trp	Glu	Tyr	Glu	Gly	Pro	
309				1075					1080					1085			
311	gag	cat	gtg	aac	ttt	tat	gtt	gaa	tat	ggg	gta	gca	ggc	agc	aaa	gaa	3435
312	Glu	His	Val	Asn	Phe	Tyr	Val	Glu	Tyr	Gly	Val	Ala	Gly	Ser	Lys	Glu	
313			1090					1095				1100					
315	gaa	tgg	aga	aaa	gaa	att	gta	aat	ggg	tct	cgg	agc	ttc	ttt	ggg	tta	3483
316	Glu	Trp	Arg	Lys	Glu	Ile	Val	Asn	Gly	Ser	Arg	Ser	Phe	Phe	Gly	Leu	
317		1105					1110				1115						
319	aag	ggg	cta	atg	cca	gga	aca	gca	tac	aaa	gtt	cga	gtt	ggg	gct	gtg	3531
320	Lys	Gly	Leu	Met	Pro	Gly	Thr	Ala	Tyr	Lys	Val	Arg	Val	Gly	Ala	Val	
321		1120				1125					1130						
323	ggg	gac	tct	ggg	ttt	gtg	agt	tca	gag	gat	gtg	ttt	gag	aca	ggc	cca	3579
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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 06/02/2006
PATENT APPLICATION: US/09/301,380A TIME: 09:38:42

Input Set : A:\PTO.txt
Output Set: N:\CRF4\06022006\I301380A.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:8; N Pos. 1

VERIFICATION SUMMARY

DATE: 06/02/2006

PATENT APPLICATION: US/09/301,380A

TIME: 09:38:42

Input Set : A:\PTO.txt

Output Set: N:\CRF4\06022006\I301380A.raw

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:700 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:0

**Raw Sequence Listing before editing
(for reference only)**



IFW16

RAW SEQUENCE LISTING

DATE: 06/01/2006

PATENT APPLICATION: US/09/301,380A

TIME: 12:11:12

Input Set: A:\20093A-21US-Substitute Sequence Listing.txt

Output Set: N:\CRF4\06012006\I301380A.raw

3 <110> APPLICANT: Murphy, Gerald P.
 4 Boynton, Alton L.
 5 Sehgal, Anil
 7 <120> TITLE OF INVENTION: Nr-CAM GENE, NUCLEIC ACIDS AND NUCLEIC ACID PRODUCTS
 8 FOR THERAPEUTIC AND DIAGNOSTIC USES FOR TUMORS
 10 <130> FILE REFERENCE: 20093A-002100US
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 18 <150> PRIOR APPLICATION NUMBER: 60/083,152
 19 <151> PRIOR FILING DATE: 1998-04-27
 21 <160> NUMBER OF SEQ ID NOS: 33
 23 <170> SOFTWARE: PatentIn Ver. 2.0

ERRORED SEQUENCES

372 <210> SEQ ID NO: 2
 373 <211> LENGTH: 1299
 374 <212> TYPE: PRT
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381 Phe	Leu	Cys	Gln	Met	Ile	Ser	Ala	Leu	Glu	Val	Pro	Leu	Asp	Pro	Lys
382			20					25				30			
384 Leu	Leu	Glu	Asp	Leu	Val	Gln	Pro	Pro	Thr	Ile	Thr	Gln	Gln	Ser	Pro
385		35					40				45				
387 Lys	Asp	Tyr	Ile	Ile	Asp	Pro	Arg	Glu	Asn	Ile	Val	Ile	Gln	Cys	Glu
388	50					55			60						
390 Ala	Lys	Gly	Lys	Pro	Pro	Pro	Ser	Phe	Ser	Trp	Thr	Arg	Asn	Gly	Thr
391 65					70				75				80		
393 His	Phe	Asp	Ile	Asp	Lys	Asp	Pro	Leu	Val	Thr	Met	Lys	Pro	Gly	Thr
394			85					90				95			
396 Gly	Thr	Leu	Ile	Ile	Asn	Ile	Met	Ser	Glu	Gly	Lys	Ala	Glu	Thr	Tyr
397		100					105				110				
399 Glu	Gly	Val	Tyr	Gln	Cys	Thr	Ala	Arg	Asn	Glu	Arg	Gly	Ala	Ala	Val
400		115					120				125				
402 Ser	Asn	Asn	Ile	Val	Val	Arg	Pro	Ser	Arg	Ser	Pro	Leu	Trp	Thr	Lys
403	130					135					140				
405 Glu	Lys	Leu	Glu	Pro	Ile	Thr	Leu	Gln	Ser	Gly	Gln	Ser	Leu	Val	Leu
406 145					150				155					160	

Does Not Comply
Corrected Diskette Needed

RAW SEQUENCE LISTING

DATE: 06/01/2006

PATENT APPLICATION: US/09/301,380A

TIME: 12:11:12

Input Set : A:\20093A-21US-Substitute Sequence Listing.txt

Output Set: N:\CRF4\06012006\I301380A.raw

```

408 Pro Cys Arg Pro Pro Ile Gly Leu Pro Pro Pro Ile Ile Phe Trp Met
409                               165                               170                               175
411 Asp Asn Ser Phe Gln Arg Leu Pro Gln Ser Glu Arg Val Ser Gln Gly
412                               180                               185                               190
414 Leu Asn Gly Asp Leu Tyr Phe Ser Asn Val Leu Pro Glu Asp Thr Arg
415                               195                               200                               205
417 Glu Asp Tyr Ile Cys Tyr Ala Arg Phe Asn His Thr Gln Thr Ile Gln
418                               210                               215                               220
420 Gln Lys Gln Pro Ile Ser Val Lys Val Ile Ser Val Asp Glu Leu Asn
421 225                               230                               235                               240
423 Asp Thr Ile Ala Ala Asn Leu Ser Asp Thr Glu Phe Tyr Gly Ala Lys
424                               245                               250                               255
426 Ser Ser Arg Glu Arg Pro Pro Thr Phe Leu Thr Pro Glu Gly Asn Ala
427                               260                               265                               270
429 Ser Asn Lys Glu Glu Leu Arg Gly Asn Val Leu Ser Leu Glu Cys Ile
430                               275                               280                               285
432 Ala Glu Gly Leu Pro Thr Pro Ile Ile Tyr Trp Ala Lys Glu Asp Gly
433                               290                               295                               300
435 Met Leu Pro Lys Asn Arg Thr Val Tyr Lys Asn Phe Glu Lys Thr Leu
436 305                               310                               315                               320
438 Gln Ile Ile His Val Ser Glu Ala Asp Ser Gly Asn Tyr Gln Cys Ile
439                               325                               330                               335
441 Ala Lys Asn Ala Leu Gly Ala Ile His His Thr Ile Ser Val Arg Val
442                               340                               345                               350
444 Lys Ala Ala Pro Tyr Trp Ile Thr Ala Pro Gln Asn Leu Val Leu Ser
445                               355                               360                               365
447 Pro Gly Glu Asp Gly Thr Leu Ile Cys Arg Ala Asn Gly Asn Pro Lys
448                               370                               375                               380
450 Pro Arg Ile Ser Trp Leu Thr Asn Gly Val Pro Ile Glu Ile Ala Pro
451 385                               390                               395                               400
453 Asp Asp Pro Ser Arg Lys Ile Asp Gly Asp Thr Ile Ile Phe Ser Asn
454                               405                               410                               415
456 Val Gln Glu Arg Ser Ser Ala Val Tyr Gln Cys Asn Ala Ser Asn Glu
457                               420                               425                               430
459 Tyr Gly Tyr Leu Leu Ala Asn Ala Phe Val Asn Val Leu Ala Glu Pro
460                               435                               440                               445
462 Pro Arg Ile Leu Thr Pro Ala Asn Thr Leu Tyr Gln Val Ile Ala Asn
463                               450                               455                               460
465 Arg Pro Ala Leu Leu Asp Cys Ala Phe Phe Gly Ser Pro Leu Pro Thr
466 465                               470                               475                               480
468 Ile Glu Trp Phe Lys Gly Ala Lys Gly Ser Ala Leu His Glu Asp Ile
469                               485                               490                               495
471 Tyr Val Leu His Glu Asn Gly Thr Leu Glu Ile Lys Asp Ala Thr Trp
472                               500                               505                               510
474 Ile Val Lys Glu Ile Pro Val Ala Gln Lys Asp Ser Thr Gly Thr Tyr
475                               515                               520                               525
477 Thr Cys Val Ala Arg Asn Lys Leu Gly Met Ala Lys Asn Glu Val His
478                               530                               535                               540
480 Leu Gln Pro Glu Tyr Ala Val Val Gln Arg Gly Ser Met Val Ser Phe

```

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```

481 545          550          555          560
483 Glu Cys Lys Val Lys His Asp His Thr Leu Ser Leu Thr Val Leu Trp
484          565          570          575
486 Leu Lys Asp Asn Arg Glu Leu Pro Ser Asp Glu Arg Phe Thr Val Asp
487          580          585          590
489 Lys Asp His Leu Val Val Ala Asp Val Ser Asp Asp Asp Ser Gly Thr
490          595          600          605
492 Tyr Thr Cys Val Ala Asn Thr Thr Leu Asp Ser Val Ser Ala Ser Ala
493          610          615          620
495 Val Leu Ser Val Val Ala Pro Thr Pro Thr Pro Ala Pro Val Tyr Asp
496 625          630          635          640
498 Val Pro Asn Pro Pro Phe Asp Leu Glu Leu Thr Asp Gln Leu Asp Lys
499          645          650          655
501 Ser Val Gln Leu Ser Trp Thr Pro Gly Asp Asp Asn Asn Ser Pro Ile
502          660          665          670
504 Thr Lys Phe Ile Ile Glu Tyr Glu Asp Ala Met His Lys Pro Gly Leu
505          675          680          685
507 Trp His His Gln Thr Glu Val Ser Gly Thr Gln Thr Thr Ala Gln Leu
508          690          695          700
510 Lys Leu Ser Pro Tyr Val Asn Tyr Ser Phe Arg Val Met Ala Val Asn
511 705          710          715          720
513 Ser Ile Gly Lys Ser Leu Pro Ser Glu Ala Ser Glu Gln Tyr Leu Thr
514          725          730          735
516 Lys Ala Ser Glu Pro Asp Lys Asn Pro Thr Ala Val Glu Gly Leu Gly
517          740          745          750
519 Ser Glu Pro Asp Asn Leu Glu Ile Thr Trp Lys Pro Leu Asn Gly Phe
520          755          760          765
522 Glu Ser Asn Gly Pro Gly Leu Gln Tyr Lys Val Ser Trp Arg Gln Lys
523          770          775          780
525 Asp Gly Asp Asp Glu Trp Thr Ser Val Val Val Ala Asn Val Ser Lys
526 785          790          795          800
528 Tyr Ile Val Ser Gly Thr Pro Thr Phe Val Pro Tyr Leu Ile Lys Val
529          805          810          815
531 Gln Ala Leu Asn Asp Met Gly Phe Ala Pro Glu Pro Ala Val Val Met
532          820          825          830
534 Gly His Ser Gly Glu Asp Leu Pro Met Val Ala Pro Gly Asn Val Arg
535          835          840          845
537 Val Asn Val Val Asn Ser Thr Leu Ala Glu Val His Trp Asp Pro Val
538          850          855          860
540 Pro Leu Lys Ser Ile Arg Gly His Leu Gln Gly Tyr Arg Ile Tyr Tyr
541 865          870          875          880
543 Trp Lys Thr Gln Ser Ser Ser Lys Arg Asn Arg Arg His Ile Glu Lys
544          885          890          895
546 Lys Ile Leu Thr Phe Gln Gly Ser Lys Thr His Gly Met Leu Pro Gly
547          900          905          910
549 Leu Glu Pro Phe Ser His Tyr Thr Leu Asn Val Arg Val Val Asn Gly
550          915          920          925
552 Lys Gly Glu Gly Pro Ala Ser Pro Asp Arg Val Phe Asn Thr Pro Glu
553          930          935          940

```

RAW SEQUENCE LISTING

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```

555 Gly Val Pro Ser Ala Pro Ser Ser Leu Lys Ile Val Asn Pro Thr Leu
556 945                      950                      955                      960
558 Asp Ser Leu Thr Leu Glu Trp Asp Pro Pro Ser His Pro Asn Gly Ile
559                      965                      970                      975
561 Leu Thr Glu Tyr Thr Leu Lys Tyr Gln Pro Ile Asn Ser Thr His Glu
562                      980                      985                      990
564 Leu Gly Pro Leu Val Asp Leu Lys Ile Pro Ala Asn Lys Thr Arg Trp
565                      995                      1000                      1005
567 Thr Leu Lys Asn Leu Asn Phe Ser Thr Arg Tyr Lys Phe Tyr Phe Tyr
568 1010                      1015                      1020
570 Ala Gln Thr Ser Ala Gly Ser Gly Ser Gln Ile Thr Glu Glu Ala Val
E--> 571 1025 / 1025                      1030                      1035                      1040
573 Thr Thr Val Asp Glu Ala Gly Ile Leu Pro Pro Asp Val Gly Ala Gly
574                      1045                      1050                      1055
576 Lys Val Gln Ala Val Asn Thr Arg Ile Ser Asn Leu Thr Ala Ala Ala
577                      1060                      1065                      1070
579 Ala Glu Thr Tyr Ala Asn Ile Ser Trp Glu Tyr Glu Gly Pro Glu His
580                      1075                      1080                      1085
582 Val Asn Phe Tyr Val Glu Tyr Gly Val Ala Gly Ser Lys Glu Glu Trp
583 1090                      1095                      1100
585 Arg Lys Glu Ile Val Asn Gly Ser Arg Ser Phe Phe Gly Leu Lys Gly
E--> 586 1105 / 1105                      1110                      1115                      1120
588 Leu Met Pro Gly Thr Ala Tyr Lys Val Arg Val Gly Ala Val Gly Asp
589                      1125                      1130                      1135
591 Ser Gly Phe Val Ser Ser Glu Asp Val Phe Glu Thr Gly Pro Ala Met
592                      1140                      1145                      1150
594 Ala Ser Arg Gln Val Asp Ile Ala Thr Gln Gly Trp Phe Ile Gly Leu
595                      1155                      1160                      1165
597 Met Cys Ala Val Ala Leu Leu Ile Leu Ile Leu Ile Val Cys Phe
598 1170                      1175                      1180
600 Ile Arg Arg Asn Lys Gly Gly Lys Tyr Pro Val Lys Glu Lys Glu Asp
E--> 601 1185 / 1185                      1190                      1195                      1200
603 Ala His Ala Asp Pro Glu Ile Gln Pro Met Lys Glu Asp Asp Gly Thr
604                      1205                      1210                      1215
606 Phe Gly Glu Tyr Ser Asp Ala Glu Asp His Lys Pro Leu Lys Lys Gly
607                      1220                      1225                      1230
609 Ser Arg Thr Pro Ser Asp Arg Thr Val Lys Lys Glu Asp Ser Asp Asp
610                      1235                      1240                      1245
612 Ser Leu Val Asp Tyr Gly Glu Gly Val Asn Gly Gln Phe Asn Glu Asp
613 1250                      1255                      1260
615 Gly Ser Phe Ile Gly Gln Tyr Ser Gly Lys Lys Glu Lys Glu Pro Ala
E--> 616 1265 / 1265                      1270                      1275                      1280
618 Glu Gly Asn Glu Ser Ser Glu Ala Pro Ser Pro Val Asn Ala Met Asn
619                      1285                      1290                      1295
621 Ser Phe Val

```

VERIFICATION SUMMARY

DATE: 06/01/2006

PATENT APPLICATION: US/09/301,380A

TIME: 12:11:14

Input Set : A:\20093A-21US-Substitute Sequence Listing.txt

Output Set: N:\CRF4\06012006\I301380A.raw

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:365 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:571 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2
L:586 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2
L:601 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2
L:616 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2
L:700 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:0